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RAW SEQUENCE LISTING                      DATE: 07/08/2002
PATENT APPLICATION:  US/10/087,188        TIME: 10:09:37

Input Set : A:\PM4978.txt
Output Set: N:\CRF3\07082002\J087188.raw
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      4 <110> APPLICANT: Rose, Steven L.
      5        Oh, Esther H.
      6        Walsh, Michael
      8 <120> TITLE OF INVENTION: Methods of Diagnosing Liver Fibrosis
     11 <130> FILE REFERENCE: P-PM 4978
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/087,188
C--> 13 <141> CURRENT FILING DATE: 2002-02-28
     13 <150> PRIOR APPLICATION NUMBER: US 10/087,188
     14 <151> PRIOR FILING DATE: 2002-02-28
     16 <160> NUMBER OF SEQ ID NOS: 4
     18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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     22 <212> TYPE: DNA
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     26 <221> NAME/KEY: CDS
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     34 atc tgt gca aac ggg cgg caa act gtg tcc tgg gca gta acc cca aag      96
     35 Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys
     36             20                  25                  30
     38 tca tta gga aat gtg aat ttc act gtg agc gca gag gca cta gag tct     144
     39 Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser
     40             35                  40                  45
     42 caa gag ctg tgt ggg act gag gtg cct tca gtt cct gaa cac gga agg     192
     43 Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg
     44         50                  55                  60
     46 aaa gac aca gtc atc aag cct ctg ttg gtt gaa cct gaa gga cta gag     240
     47 Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu
     48 65                  70                  75                  80
     50 aag gaa aca aca ttc aac tcc cta ctt tgt cca tca ggt ggt gag gtt     288
     51 Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val
     52             85                  90                  95
     54 tct gaa gaa tta tcc ctg aaa ctg cca cca aat gtg gta gaa gaa tct     336
     55 Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser
     56             100                 105                 110
     58 gcc cga gct tct gtc tca gtt ttg gga gac ata tta ggc tct gcc atg     384
     59 Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met
     60         115                 120                 125
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62 caa aac aca caa aat ctt ctc cag atg ccc tat ggc tgt gga gag cag   432
63 Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln
64     130             135             140
66 aat atg gtc ctc ttt gct cct aac atc tat gta ctg gat tat cta aat   480
67 Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn
68 145             150             155             160
70 gaa aca cag cag ctt act cca gag atc aag tcc aag gcc att ggc tat   528
71 Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr
72             165             170             175
74 ctc aac act ggt tac cag aga cag ttg aac tac aaa cac tat gat ggc   576
75 Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly
76             180             185             190
78 tcc tac agc acc ttt ggg gag cga tat ggc agg aac cag ggc aac acc   624
79 Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr
80             195             200             205
82 tgg ctc aca gcc ttt gtt ctg aag act ttt gcc caa gct cga gcc tac   672
83 Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr
84     210             215             220
86 atc ttc atc gat gaa gca cac att acc caa gcc ctc ata tgg ctc tcc   720
87 Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser
88 225             230             235             240
90 cag agg cag aag gac aat ggc tgt ttc agg agc tct ggg tca ctg ctc   768
91 Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu
92             245             250             255
94 aac aat gcc ata aag gga gga gta gaa gat gaa gtg acc ctc tcc gcc   816
95 Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala
96             260             265             270
98 tat atc acc atc gcc ctt ctg gag att cct ctc aca gtc act cac cct   864
99 Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro
100     275             280             285
102 gtt gtc cgc aat gcc ctg ttt tgc ctg gag tca gcc tgg aag aca gca   912
103 Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala
104     290             295             300
106 caa gaa ggg gac cat ggc agc cat gta tat acc aaa gac ctg ctg gcc   960
107 Gln Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Asp Leu Leu Ala
108 305             310             315             320
110 tat gct ttt gcc ctg gca ggt aac cag gac aag agg aag gaa gta ctc   1008
111 Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu
112             325             330             335
114 aag tca ctt aat gag gaa gct gtg aag aaa gac aac tct gtc cat tgg   1056
115 Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp
116             340             345             350
118 gag cgc cct cag aaa ccc aag gca cca gtg ggg gat ttt tac gaa ccc   1104
119 Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly Asp Phe Tyr Glu Pro
120             355             360             365
122 cag gct ccc tct gct gag gtg gag atg aca tcc tat gtg ctc ctc gct   1152
123 Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala
124     370             375             380
126 tat ctc acg gcc cag cca gcc cca acc tcg gag gac ctg acc tct gca   1200
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127 Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala
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130 acc aac atc gtg aag tgg atc acg aag cag cag aat gcc cag ggc ggt  1248
131 Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly
132             405             410             415
134 ttc tcc tcc acc cag gac aca gtg gtg gct ctc cat gct ctg tcc aaa  1296
135 Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys
136             420             425             430
138 tat gga gca gcc aca ttt acc agg act ggg aag gct gca cag gtg act  1344
139 Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr
140         435             440             445
142 atc cag tct tca ggg aca ttt tcc agc aaa ttc caa gtg gac aac aac  1392
143 Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn
144         450             455             460
146 aac cgc ctg tta ctg cag cag gtc tca ttg cca gag ctg cct ggg gaa  1440
147 Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu
148 465             470             475             480
150 tac agc atg aaa gtg aca gga gaa gga tgt gtc tac ctc cag aca tcc  1488
151 Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser
152             485             490             495
154 ttg aaa tac aat att ctc cca gaa aag gaa gag ttc ccc ttt gct tta  1536
155 Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu
156             500             505             510
158 gga gtg cag act ctg cct caa act tgt gat gaa ccc aaa gcc cac acc  1584
159 Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr
160         515             520             525
162 agc ttc caa atc tcc cta agt gtc agt tac aca ggg agc cgc tct gcc  1632
163 Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala
164         530             535             540
166 tcc aac atg gcg atc gtt gat gtg aag atg gtc tct ggc ttc att ccc  1680
167 Ser Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro
168 545             550             555             560
170 ctg aag cca aca gtg aaa atg ctt gaa aga tct aac cat gtg agc cgg  1728
171 Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg
172             565             570             575
174 aca gaa gtc agc agc aac cat gtc ttg att tac ctt gat aag gtg tca  1776
175 Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser
176             580             585             590
178 aat cag aca ctg agc ttg ttc ttc acg gtt ctg caa gat gtc cca gta  1824
179 Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val
180         595             600             605
182 aga gat ctg aaa cca gcc ata gtg aaa gtc tat gat tac tac gag acg  1872
183 Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr
184     610             615             620
186 gat gag ttt gca att gct gag tac aat gct cct tgc agc aaa gat ctt  1920
187 Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu
188 625             630             635             640
190 gga aat gct tga agaccacaag gctgaaaagt gctttgctgg agtcctgttc      1972
191 Gly Asn Ala *
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207 Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser
208         35                  40                  45
209 Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg
210     50                  55                  60
211 Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu
212 65                  70                  75                  80
213 Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val
214                 85                  90                  95
215 Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser
216             100                 105                 110
217 Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met
218         115                 120                 125
219 Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln
220     130                 135                 140
221 Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn
222 145                 150                 155                 160
223 Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile Gly Tyr
224                 165                 170                 175
225 Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly
226             180                 185                 190
227 Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr
228         195                 200                 205
229 Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr
230     210                 215                 220
231 Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser
232 225                 230                 235                 240
233 Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu
234                 245                 250                 255
235 Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala
236             260                 265                 270
237 Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro
238     275                 280                 285
239 Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala
240     290                 295                 300
241 Gln Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Asp Leu Leu Ala
242 305                 310                 315                 320
243 Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu
244             325                 330                 335
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245 Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp
246             340             345             350
247 Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly Asp Phe Tyr Glu Pro
248         355             360             365
249 Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala
250     370             375             380
251 Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala
252 385             390             395             400
253 Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly
254             405             410             415
255 Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys
256         420             425             430
257 Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr
258     435             440             445
259 Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn
260     450             455             460
261 Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu
262 465             470             475             480
263 Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser
264             485             490             495
265 Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu
266         500             505             510
267 Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr
268     515             520             525
269 Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala
270     530             535             540
271 Ser Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro
272 545             550             555             560
273 Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg
274             565             570             575
275 Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser
276             580             585             590
277 Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val
278         595             600             605
279 Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr
280     610             615             620
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VERIFICATION SUMMARY   DATE: 07/08/2002
PATENT APPLICATION: **US/10/087,188**   TIME: 10:09:38

Input Set : **A:\PM4978.txt**
Output Set: **N:\CRF3\07082002\J087188.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:354 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3